WEST Search History

| Hide Items | Restore | Clear | Cancel |

DATE: Tuesday, November 09, 2004

Hide?	Set Name	Query	Hit Count
		DB=USPT; PLUR=YES; OP=AND	
☐	L1	glycosyltransferase or glycosyl-transferase	949
☐	L2	L1 same sucrose	39
☐	L3	L1 same sucros$	40
☐	L4	L1.clm. and method.clm. and (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm.	2
☐	L5	L1 near25 (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm.	1
		DB=EPAB,JPAB,DWPI; PLUR=YES; OP=AND	
☐	L6	glycosyltransferase or glycosyl-transferase	416
☐	L7	L6 near25 (inhibitor or inactivator or inhibition or regulator or modulator or modulates or antagonists or antagonize or antagonise or blocker or blocks or blocked).clm.	0

END OF SEARCH HISTORY

```
### Status: Signed Off. (1 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009998...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.16.00D

Last logoff:  06oct04 11:13:23
Logon file405 06oct04 14:21:51
* * *
SYSTEM:HOME
Cost is in DialUnits
Menu System II: D2 version 1.7.9 term=ASCII
                    *** DIALOG HOMEBASE(SM) Main Menu ***


 Information:
  1.  Announcements (new files, reloads, etc.)
  2.  Database, Rates, & Command Descriptions
  3.  Help in Choosing Databases for Your Topic
  4.  Customer Services (telephone assistance, training, seminars, etc.)
  5.  Product Descriptions

 Connections:
  6.  DIALOG(R) Document Delivery
  7.  Data Star(R)

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     /H = Help            /L = Logoff           /NOMENU = Command Mode


Enter an option number to view information or to connect to an online
 service.  Enter a BEGIN command plus a file number to search a database
(e.g., B1 for ERIC).
?b 155

      06oct04 14:21:52 User228206 Session D2253.1
          $0.00    0.200 DialUnits FileHomeBase
     $0.00  Estimated cost FileHomeBase
     $0.00  Estimated cost this search
     $0.00  Estimated total session cost   0.200 DialUnits


File 155:MEDLINE(R) 1951-2004/Oct W1
      (c) format only 2004 The Dialog Corp.
*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.

     Set  Items  Description
     ---  -----  -----------
?e quorum sensing

Ref    Items  Index-term
E1        14  QUOROM
```

```
E2        851   QUORUM
E3          0  *QUORUM SENSING
E4          1   QUORUMQUENCHING
E5          2   QUORUMS
E6          1   QUORUMSENSING
E7          1   QUOSO
E8          3   QUOT
E9        823   QUOTA
E10        10   QUOTABLE
E11         1   QUOTACP
E12         3   QUOTANE

        Enter P or PAGE for more
?s e6
      S1        1   'QUORUMSENSING'
?s quor? (3n) sens?
            882   QUOR?
         832533   SENS?
      S2      780   QUOR? (3N) SENS?
?e autoinducer

Ref   Items   Index-term
E1       11   AUTOINDUCE
E2       26   AUTOINDUCED
E3      302  *AUTOINDUCER
E4      106   AUTOINDUCERS
E5        6   AUTOINDUCES
E6       17   AUTOINDUCIBLE
E7        1   AUTOINDUCIBLY
E8        2   AUTOINDUCIDA
E9        1   AUTOINDUCIDO
E10      28   AUTOINDUCING
E11       1   AUTOINDUCTIBILITY
E12     341   AUTOINDUCTION

        Enter P or PAGE for more
?s autoinduc?
      S3      748   AUTOINDUC?
?ds

Set    Items   Description
S1         1   'QUORUMSENSING'
S2       780   QUOR? (3N) SENS?
S3       748   AUTOINDUC?
?s s1 or s2 or s3
              1   S1
            780   S2
            748   S3
      S4     1310   S1 OR S2 OR S3
?e succrose

Ref   Items   Index-term
E1        1   SUCCR
E2        1   SUCCRALFAT
E3        7  *SUCCROSE
E4        2   SUCCS
E5        1   SUCCSES
E6        1   SUCCSSFULLY
E7        1   SUCCTION
E8        1   SUCCUBANCE
E9        2   SUCCUBANZA
E10       1   SUCCUBANZE
E11       1   SUCCUBI
E12       1   SUCCUDANEOUS

        Enter P or PAGE for more
?s e3
```

```
      S5        7  'SUCCROSE'
?s sucrose
      S6    41264  SUCROSE
?e sucrose

Ref    Items    RT  Index-term
E1        4          SUCROS
E2        2          SUCROSA
E3    41264     6  *SUCROSE
E4       13          SUCROSE - FRUCTAN 6-FRUCTOSYLTRANSFERASE
E5     1390          SUCROSE --ADMINISTRATION AND DOSAGE --AD
E6      665          SUCROSE --ADVERSE EFFECTS --AE
E7      469          SUCROSE --ANALOGS AND DERIVATIVES --AA
E8      475          SUCROSE --ANALYSIS --AN
E9       35          SUCROSE --ANTAGONISTS AND INHIBITORS --AI
E10      52          SUCROSE --BIOSYNTHESIS --BI
E11     113          SUCROSE --BLOOD --BL
E12      23          SUCROSE --CEREBROSPINAL FLUID --CF

        Enter P or PAGE for more
?s sucrose?
      S7    41279  SUCROSE?
?ds

Set    Items    Description
S1        1     'QUORUMSENSING'
S2      780     QUOR? (3N) SENS?
S3      748     AUTOINDUC?
S4     1310     S1 OR S2 OR S3
S5        7     'SUCCROSE'
S6    41264     SUCROSE
S7    41279     SUCROSE?
?s s4 (25n) (s5 or s6 or s7)
           1310   S4
              7   S5
          41264   S6
          41279   S7
      S8        0   S4 (25N) (S5 OR S6 OR S7)
?s s4 and (s5 or s6 or s7)
           1310   S4
              7   S5
          41264   S6
          41279   S7
      S9        1   S4 AND (S5 OR S6 OR S7)
?t s9/9/all
```

9/9/1
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

16188354   PMID: 15090509
  **LuxS-mediated signaling in Streptococcus mutans is involved in regulation
of acid and oxidative stress tolerance and biofilm formation.**
  Wen Zezhang T; Burne Robert A
  Department of Oral Biology, College of Dentistry, University of Florida,
Gainesville, FL 32610, USA.
  Journal of bacteriology (United States)   May 2004,   186 (9) p2682-91,
ISSN 0021-9193   Journal Code: 2985120R
  Contract/Grant No.: DE 12236; DE; NIDCR; DE 13239; DE; NIDCR; DE 15501;
DE; NIDCR
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Subfile: INDEX MEDICUS
  LuxS-mediated   **quorum   sensing**   has   recently been shown to regulate
important physiologic functions and virulence in a variety of bacteria. In

this study, the role of luxS of Streptococcus mutans in the regulation of traits crucial to pathogenesis was investigated. Reporter gene fusions showed that inactivation of luxS resulted in a down-regulation of fructanase, a demonstrated virulence determinant, by more than 50%. The LuxS-deficient strain (TW26) showed increased sensitivity to acid killing but could still undergo acid adaptation. Northern hybridization revealed that the expression of RecA, SmnA (AP endonuclease), and Nth (endonuclease) were down-regulated in TW26, especially in early-exponential-phase cells. Other down-regulated genes included ffh (a signal recognition particle subunit) and brpA (biofilm regulatory protein A). Interestingly, the luxS mutant showed an increase in survival rate in the presence of hydrogen peroxide (58.8 mM). The luxS mutant formed less biofilm on hydroxylapatite disks, especially when grown in biofilm medium with **sucrose** , and the mutant biofilms appeared loose and hive-like, whereas the biofilms of the wild type were smooth and confluent. The mutant phenotypes were complemented by exposure to supernatants from wild-type cultures. Two loci, smu486 and smu487, were identified and predicted to encode a histidine kinase and a response regulator. The phenotypes of the smu486 smu487 mutant were, in almost all cases, similar to those of the luxS mutant, although our results suggest that this is not due to AI-2 signal transduction via Smu486 and Smu487. This study demonstrates that luxS-dependent signaling plays critical roles in modulating key virulence properties of S. mutans.
   Tags: Support, U.S. Gov't, P.H.S.
   Descriptors: *Bacterial Proteins--physiology--PH; *Biofilms--growth and development--GD; *Oxidative Stress; *Signal Transduction; *Streptococcus mutans--physiology--PH; Hydrogen-Ion Concentration; Regulon; Virulence --genetics--GE
   CAS Registry No.: 0   (Bacterial Proteins); 0   (LuxS protein, Bacteria)
   Record Date Created: 20040419
   Record Date Completed: 20040520
?logoff hold
         06oct04 14:23:47 User228206 Session D2253.2
            $5.14   1.607 DialUnits File155
              $0.21 1 Type(s) in Format 9
            $0.21 1 Types
     $5.35   Estimated cost File155
     $0.50   TELNET
     $5.85   Estimated cost this search
     $5.85   Estimated total session cost   1.807 DialUnits

Status: Signed Off. (2 minutes)

Status: Path 1 of [Dialog Information Services via Modem]

Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009998...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
Status: Signing onto Dialog
 ****
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
Status: Connected

Dialog level 04.16.00D

Reconnected in file 155 06oct04 14:24:43
* * *

File 155:MEDLINE(R) 1951-2004/Oct W1
      (c) format only 2004 The Dialog Corp.

```
        Set   Items   Description
        ---   -----   -----------
Cost is in DialUnits
?ds

Set      Items     Description
S1           1     'QUORUMSENSING'
S2         780     QUOR? (3N) SENS?
S3         748     AUTOINDUC?
S4        1310     S1 OR S2 OR S3
S5           7     'SUCCROSE'
S6       41264     SUCROSE
S7       41279     SUCROSE?
S8           0     S4 (25N) (S5 OR S6 OR S7)
S9           1     S4 AND (S5 OR S6 OR S7)
?s mutans? (25n) sucros?
          5898     MUTANS?
         41283     SUCROS?
    S10    697     MUTANS? (25N) SUCROS?
?s s10 and (capsul? or media or medium?)
           697     S10
         50357     CAPSUL?
        210895     MEDIA
        205746     MEDIUM?
    S11    123     S10 AND (CAPSUL? OR MEDIA OR MEDIUM?)
?s s11/2000:2004
           123     S11
       2510633     PY=2000 : PY=2004
    S12     28     S11/2000:2004
?s s11 not s12
           123     S11
            28     S12
    S13     95     S11 NOT S12
?target s13/all
Your TARGET search request will retrieve up to 50 of the statistically most
relevant records.
Searching ALL records
...Processing Complete
    S14     50     TARGET - S13
Ending TARGET search. Enter TARGET to do another search in the present
file(s), or BEGIN new file(s).  Enter LOGOFF to disconnect from Dialog
?t s14/9/all
```

14/9/1
DIALOG(R)File 155:MEDLINE(R)
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08367460   PMID: 2532001
  The   influence of Streptococcus mutans on adhesion of Candida albicans to
acrylic surfaces in vitro.
  Branting C; Sund M L; Linder L E
  Department of Oral Microbiology, Huddinge University Hospital, Karolinska
Institute, Sweden.
  Archives   of   oral   biology (ENGLAND)   1989,   34   (5)   p347-53,   ISSN
0003-9969   Journal Code: 0116711
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Subfile: DENTAL; INDEX MEDICUS
  Adhesion of Candida albicans and Streptococcus mutans was studied by
incubation of radiolabelled cells with acrylic test specimens in a
chemically defined growth medium. Strep. mutans adhered firmly in the
presence of   **sucrose** , while C. albicans was only loosely attached to the

🏠 **ExPASy Home page**	**Site Map**	**Search ExPASy**	**Contact us**	**Swiss-Prot**

Search [Swiss-Prot/TrEMBL ▼] for [autoinducer mutans   ] [Go] [Clear]

NiceProt View of TrEMBL: Q99QI5

[Printer-friendly view] [Request update] [Quick BlastP search]

[**Entry info**] [**Name and origin**] [**References**] [**Comments**] [**Cross-references**] [**Keywords**]
[**Features**] [**Sequence**] [**Tools**]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q99QI5**
Primary accession number	**Q99QI5**
Secondary accession number	Q7CE98
Entered in TrEMBL in	Release 17, June 2001
Sequence was last modified in	Release 17, June 2001
Annotations were last modified in	Release 28, October 2004

Name and origin of the protein

|	
Protein name	**Competence stimulating protein**
Synonym	**Competence stimulating peptide,**
Gene name	**Name: comC**
	OrderedLocusNames: SMU.1915
From	Streptococcus mutans [TaxID: 1309]
Taxonomy	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

References

[1] SEQUENCE FROM NUCLEIC ACID.
    STRAIN=GB14, H7, LT11, NG8, and UA159;
    DOI=10.1128/JB.183.3.897-908.2001;MEDLINE=21142515;PubMed=11208787 [NCBI, ExPASy, EBI, Israel, Japan]
    Li Y.H., Lau P.C.Y., Lee J.H., Ellen R.P., Cvitkovitch D.G.;
    "Natural genetic transformation of Streptococcus mutans growing in biofilms.";
    J. Bacteriol. 183:897-908(2001).

[2] SEQUENCE FROM NUCLEIC ACID.
    STRAIN=UA159 / ATCC 700610 / Serotype c;
    DOI=10.1073/pnas.172501299;MEDLINE=22295063;PubMed=12397186 [NCBI, ExPASy, EBI, Israel, Japan]
    Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A., Ferretti J.J.;
    "Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen.";
    Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

Comments

None

Cross-references

EMBL	AF277152; AAK01542.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF277153; AAK01543.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF277155; AAK01545.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF277156; AAK01546.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF277157; AAK01547.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AE015016; AAN59526.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	Q99QI5; SMU.1915.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q99QI5.
PRESAGE	Q99QI5.
ModBase	Q99QI5.
SMR	Q99QI5; 38FA62B6F78FC3BF.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome.

Features
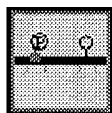
 Feature table viewer

```
Key      From  To  Length   Description
CHAIN     26   46    21     competence stimulating protein.
```

Sequence information

Length: **46 AA** [This is the length of the unprocessed precursor]

Molecular weight: **5211 Da** [This is the MW of the unprocessed precursor]

CRC64: **38FA62B6F78FC3BF** [This is a checksum on the sequence]

```
         10        , 20         30        40
          |           |          |         |
MKKTLSLKND FKEIKTDELE IIIGGSGSLS TFFRLFNRSF TQALGK
```

Q99QI5 in FASTA format

View entry in original TrEMBL format
View entry in raw text format (no links)
Request for annotation of this TrEMBL entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

ExPASy Home page | **Site Map** | **Search ExPASy** | **Contact us** | **Proteomics tools** | **Swiss-Prot**

Search Swiss-Prot/TrEMBL ▼ for autoinducer mutans Go Clear

===

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that
the computation was performed at the SIB using the BLAST network service.
The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

===

Query length: 21 AA
Date run: 2004-11-09 12:04:31 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
        1,621,919 sequences; 518,174,383 total letters

  Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) ▼ Submit Query
  Select up to...

☐ Include query sequence

```
    Db AC       Description                                            Score E-value

☐  tr Q99QI5 Competence stimulating protein (Competence stimulating... 68 2e-11
☐  tr Q9APK7 Competence stimulating protein [comC] [Streptococcus m... 68 2e-11
☐  tr Q9APK6 Competence stimulating protein [comC] [Streptococcus m... 57 4e-08
☐  tr Q7UJT6 Acriflavine resistance protein B [acrB] [Rhodopirellul... 32  1.4
☐  sp P38771 FIL1_YEAST FIL1 protein, mitochondrial precursor [FIL1... 30  4.5
☐  tr Q7SAC2 Predicted protein [NCU06309.1] [Neurospora crassa]       30  4.5
☐  tr Q8EL34 Hypothetical conserved protein [OB3397] [Oceanobacillu... 29  8.0
```
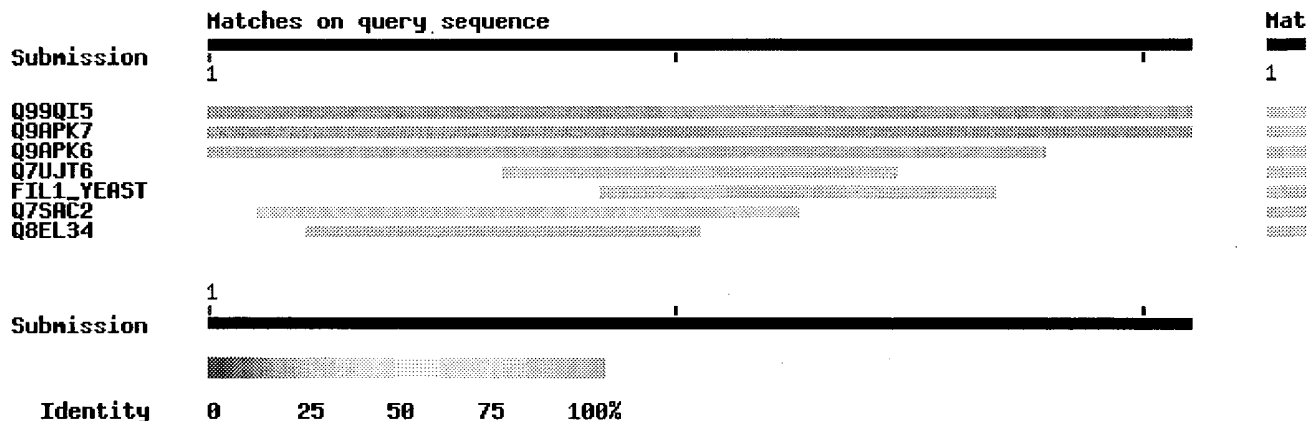
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs
(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

Matches on query sequence   Mat

Submission
1   1

Q99QI5
Q9APK7
Q9APK6
Q7UJT6
FIL1_YEAST
Q7SAC2
Q8EL34

Submission
1

Identity   0   25   50   75   100%

Alignments

tr Q99QI5 Competence stimulating protein (Competence stimulating   46 AA
           peptide,)
           [comC] [Streptococcus mutans]   align

 Score = 67.7 bits (152), Expect = 2e-11
 Identities = 21/21 (100%), Positives = 21/21 (100%)

Query: 1   SGSLSTFFRLFNRSFTQALGK 21
           SGSLSTFFRLFNRSFTQALGK
Sbjct: 26 SGSLSTFFRLFNRSFTQALGK 46

tr Q9APK7 Competence stimulating protein [comC] [Streptococcus mutans] 46 AA

                                                                           align

 Score = 67.7 bits (152), Expect = 2e-11
 Identities = 21/21 (100%), Positives = 21/21 (100%)

Query: 1   SGSLSTFFRLFNRSFTQALGK 21
           SGSLSTFFRLFNRSFTQALGK
Sbjct: 26 SGSLSTFFRLFNRSFTQALGK 46

tr Q9APK6 Competence stimulating protein [comC] [Streptococcus mutans] 43 AA

                                                                           align

```
Score = 56.6 bits (126), Expect = 4e-08
Identities = 17/18 (94%), Positives = 17/18 (94%)

Query: 1   SGSLSTFFRLFNRSFTQA 18
           SG LSTFFRLFNRSFTQA
Sbjct: 26  SGTLSTFFRLFNRSFTQA 43
```

tr Q7UJT6 **Acriflavine resistance protein B [acrB] [Rhodopirellula**   1072
            baltica]   AA
                                                                                 align

```
Score = 31.6 bits (67), Expect = 1.4
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 7    FFRLFNRSF 15
            FFRLFNR F
Sbjct: 540  FFRLFNRTF 548
```

sp P38771   **FIL1 protein, mitochondrial precursor [FIL1]**   230
    FIL1_YEAST   **[Saccharomyces**   AA
                 cerevisiae (Baker's yeast)]   align

```
Score = 29.9 bits (63), Expect = 4.5
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 9   RLFNRSFTQ 17
           RLFNRSF Q
Sbjct: 17  RLFNRSFSQ 25
```

tr Q7SAC2 **Predicted protein [NCU06309.1] [Neurospora crassa]**   699 AA

                                                                     align

```
Score = 29.9 bits (63), Expect = 4.5
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 2    GSLSTFFRLFNR 13
            GS STF RLFNR
Sbjct: 422  GSPSTFMRLFNR 433
```

tr Q8EL34 **Hypothetical conserved protein [OB3397] [Oceanobacillus**   268
            iheyensis]   AA
                                                                                 align

```
Score = 29.1 bits (61), Expect = 8.0
Identities = 8/9 (88%), Positives = 9/9 (99%)
```

```
Query: 3    SLSTFFRLF 11
            SLSTF+RLF
Sbjct: 242  SLSTFYRLF 250
```

```
Database: EXPASY/UniProt
    Posted date:  Nov 8, 2004  3:52 PM
  Number of letters in database: 518,174,383
  Number of sequences in database:  1,621,919

Lambda     K       H
   0.348    0.289    1.75

Gapped
Lambda     K       H
   0.294    0.110    0.610


Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 21
length of database: 518,174,383
effective HSP length: 12
effective length of query: 9
effective length of database: 498,711,355
effective search space: 4488402195
effective search space used: 4488402195
T: 16
A: 40
X1: 14 ( 7.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (21.9 bits)
S2: 61 (29.1 bits)
```

NCBI   **PubMed**   National Library of Medicine **NLM**

Entrez   PubMed   Nucleotide   Protein   Genome   Structure   OMIM   PMC   Journals   Boo

Search PubMed ▼ for archives of oral biology 2000 cariostatic   Go   Clear

Limits   Preview/Index   History   Clipboard   Details

Display Summary ▼ Show: 20 ▼ Sort ▼ Send to

Items 1 - 11 of 11

☐ **1:** Ooshima T, Osaka Y, Sasaki H, Osawa K, Yasuda H, Matsumoto M.   Relate

Cariostatic activity of cacao mass extract.
Arch Oral Biol. 2000 Sep;45(9):805-8.
PMID: 10869494 [PubMed - indexed for MEDLINE]

☐ **2:** Ooshima T, Osaka Y, Sasaki H, Osawa K, Yasuda H, Matsumura M, Sobue S,   Relate
Matsumoto M.

Caries inhibitory activity of cacao bean husk extract in in-vitro and animal e
Arch Oral Biol. 2000 Aug;45(8):639-45.
PMID: 10869475 [PubMed - indexed for MEDLINE]

☐ **3:** Rose RK.   Relate

Effects of an anticariogenic casein phosphopeptide on calcium diffusion in s
model dental plaques.
Arch Oral Biol. 2000 Jul;45(7):569-75.
PMID: 10785520 [PubMed - indexed for MEDLINE]

☐ **4:** Larsen MJ, Pearce EI, Ravnholt G.   Relate

Dissolution of powdered human enamel suspended in acid solutions at a high
solid/solution ratio under a 5% CO_2 atmosphere at 20 degrees C.
Arch Oral Biol. 1997 Sep;42(9):657-63.
PMID: 9403120 [PubMed - indexed for MEDLINE]

☐ **5:** Tyler JE, Poole DF.   Relate

Uptake of fluoride by human surface enamel from ammonium bifluoride and
reduction in the penetration in vitro by caries-like lesions.
Arch Oral Biol. 1984;29(12):971-4.
PMID: 6598366 [PubMed - indexed for MEDLINE]

☐ **6:** Hayes ML.   Relate

The inhibition of bacterial glycolysis in human dental plaque by medium-ch:
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